

novel EGIII-like cellulase of *Streptomyces* sp. J168. It was deduced from a gene sequence isolated from genomic DNA using PCR primers (see AAY06310-9) based on conserved motifs (see AAY06325-29) of *Trichoderma reesei* EGIII-like cellulase and related enzymes. For best results used to identify novel EGIII-like enzymes, including the present product, from bacterial and fungal sources (see AAY06310-70), the sequence shows homology to *T. reesei* EGIII (see AAY06330). Also provided by the inventor are vectors, host cells and methods for the production of such enzymes, which can be used in the treatment of cellulose containing textiles, as food additives in the treatment of wood pulp, in the reduction of biomass to glucose, in the stonewashing of indigo dyed denim, or as laundry detergent components (all claimed).

Sequence: 471 AA.

Query Match 62.4% Score 43 DB 21 Length 471
 Local Similarity 62.7% Ident. No. 40
 Matches 8 Conserved 15 Mismatches 3 Indels 0 Gaps 0
 2 AM030483886.14
 1 111 111
 657 apdqatlnrso qqr

RESULT 2

AA013900 standard; Protein: 471 AA.

AA013900
 AA013900
 21 NOV 2000 (first entry)
 Streptomyces lividans strain EGIII-like cellulase.
 Streptomyces lividans: *Trichoderma reesei*: endoglucanase III: EGIII: cellulase; mutant: enzyme stability; textile treatment; wood pulp treatment; feed additively detergent.
 Streptomyces lividans.
 W020004614 A2.

29 JUN 2000.
 12 NOV 1999. 99WO 0524704.
 18 DEC 1998. 98OS 0162796.
 (GENEV) GENEWORK INT INC.

Multidomain 2: Wood 141

WPI: 2000 40439742.

Novel endoglucanase III or endoglucanase III-like cellulase useful for treating textiles and wood pulp comprises a substituted or deleted at specified positions in the wild form of endoglucanase III.

Example 1: Fig 3: 4pp: English.

The present sequence is a cellulase related to endoglucanase III (EGIII) from *Trichoderma reesei*. EGIII-like genes were isolated from genomic DNA libraries constructed from various microorganisms by PCR. The isolated genes showed significant homology to EGIII from *T. reesei*. Cellulase substitution and deletion mutations have been incorporated into EGIII and EGIII-like cellulases to produce variant enzymes with improved stability, e.g., increased resistance to temperature stress, the mutants may be used in textile and wood pulp treatment as a food additive, and for reducing biomass to glucose. They are also useful for stonewashing or indigo dyed denim and as an agent in laundry and dish detergents.

Sequence: 471 AA.

Query Match 62.4% Score 43 DB 21 Length 471
 Local Similarity 62.7% Ident. No. 40
 Matches 8 Conserved 15 Mismatches 3 Indels 0 Gaps 0
 2 AM030483886.14
 1 111 111
 657 apdqatlnrso qqr

RESULT 4

AA064445 standard; Protein: 471 AA.

AA064445
 AA064445
 12 JUL 2000 (first entry)

Amino acid sequence of an endoglucanase III (EGIII) like cellulase.

Endoglucanase III: EGIII: EGIII-like cellulase; surfactant stability; cellulase; textile processing; textile cleaning; stonewashing; indigo dyed denim; cellulase containing fabric; fabric smoothening; fill removal; fill removal; cellulase cellulase fiber dyeing detergent; animal feed; wood pulp; paper; grain; biomass; reducing glucose.

Actinomyces sp.
 W020014208 A1.
 16 MAR 2000.
 24 AUG 1999. 99WO 0519154.
 03 SEP 1998. 98OS 0146729.

(GENEV) GENEWORK INT INC.

Fowler T.

WPI: 2000 271052734.

Novel variant endoglucanase III-like cellulases with improved surfactant stability and resistance to temperature stress, useful for textile processing or cleaning, treating wood pulp, food and grain, and reducing biomass to glucose.

Disclosure: Page 64 65: 7pp: English.

The present sequence represents an endoglucanase III (EGIII)-like cellulase. The cellulase has homology to the *Trichoderma reesei* EGIII protein. The variant cellulases have improved temperature stability, and improved enzyme stability. The variant cellulases and compositions containing them are used in textile processing or cleaning, e.g., stonewashing of indigo dyed denim, and modifying the texture, feel or appearance of cellulase containing fabrics (e.g., improving fabric smoothness or removing pills and fibrils). The compositions may also be used for the removal of immature or dead cotton from cellulosic fibres or fabric, which can cause uneven dyeing. The cellulase may also be used in a detergent composition for washing laundry and dishes and in the treatment of animal feed, wood pulp, paper, non-animal foods and stains. The enzymes may also be used in the reduction of biomass to glucose.

Sequence: 471 AA.

Query Match 62.4% Score 43 DB 21 Length 471
 Local Similarity 62.7% Ident. No. 40
 Matches 8 Conserved 15 Mismatches 3 Indels 0 Gaps 0
 2 AM030483886.14

1 1111 1111
 357 apdqqlnatsc 108

RESULT 4

AAV67497

AAV67497 standard: Protein: 386 AA.

AC AAV67497:

D1 19-MAY-2000 (first entry)

DE Protein sequence of Cc1A and cellulase 11A68 fusion.

Cellulase: Actinomyces detergent; food additive; textile treatment;

pulp; paper; cellulase 11A68.

Streptomyces lividans.

Synthetic.

Key: 100% identity

F1 Peptide:

1-46

F1 /note: "Cc1A signal sequence"

F1 Protein:

47-136

F1 /note: "cellulase 11A68 mature peptide"

PN W020009707-A1.

PD 24-FEB-2000.

PE 28-MAY-1999: 69W-0111971.

PF 24-JUN-1998: 980S-0104508.

PG 18-NOV-1998: 980S-0524649.

PK 28-MAY-1999: 990S-0421981.

PL (GENE) GENEMOR INT INC.

PJ Jones RE, Van der Kleij WH, Van Solingen P, Weijer W;

PK WPI: 2-000-224444/1.

PL N-Peptide AAV67031.

A novel Actinomyces cellulase and related DNA, useful for detergent

compositions, treating textiles and paper or pulp.

Example 6; Fig 15; 72pp; English.

The invention provides a cellulase from Actinomyces. The cellulase can

be used in a detergent composition, as an additive for animal feed and

for the treatment of textiles or pulp and paper. The DNA encoding the

cellulase can be used to identify hemolysins, cellulases and for

recombinant production of cellulases. The present sequence represents

the protein sequence of a Cc1A signal sequence and cellulase 11A68

fusion sequence contained in the expression cassette consisting of the

G1 promoter, Cc1A signal sequence, cellulase 11A68 and G1 terminator

Sequence: 386 AA:

Query Match: 62.8% Score 43; DB 21; Length 386;
 Best Local Similarity: 66.7% (Frag. No. 41)
 Matches: 8; Conservatio: 1; Mismatches: 3; Indels: 0; Gaps: 0

QY 2 AMGGREKSSSC 14

ID 1 1111 11 1

ID 372 apdqqlnatsc 108

RESULT 5
 AAB39255
 ID AAB39255 standard: Protein: 33 AA.

AC AAB39255:

D1 02-FEB-2001 (first entry)

DE Gene 17 human secreted protein, function unknown; 133

Human secreted protein 17 (hSP17) is a secreted protein that is

antiproliferative, cytostatic, and has been shown to be involved in

neuroprotection, neuroprotection, and has been shown to be involved in

opthalmological and immunological diseases. The gene of hSP17 and hSP17

hyperproliferative disorder (hSP17-HPD) is a rare genetic disorder

characterized by hyperproliferative disorder (hSP17-HPD) is a rare

wound healing disorder (hSP17-HPD) is a rare genetic disorder

Mus musculus.

W02000956704-A1.

28-SEP-2000.

16-MAR-2000: 200W-1806704.

19-MAR-1999: 990S-0421981.

10-DEC-1999: 990S-0524649.

(HUMAN) HUMAN GENE SEI INC.

Kosov GA, Buden SM, Komarova IS;

WPI: 2000 579433/96.

Isolated nucleic acid molecule encoding a protein, secreted protein

used to prevent the treatment of a hyperproliferative disorder

Disclosures: Page 44; English.

The polypeptide sequences of hSP17 and hSP17 are encoded by the human

secreted protein 17 (hSP17) gene, which is located on chromosome 17p11.2.

AAB39255 and AAB39256 are alternative splicing variants of the hSP17

protein sequences. While hSP17 and hSP17 have been shown to be

involved in neuroprotection, neuroprotection, and has been shown to be

involved in opthalmological and immunological diseases. The gene of

hSP17 and hSP17 hyperproliferative disorder (hSP17-HPD) is a rare

genetic disorder characterized by hyperproliferative disorder (hSP17-

HPD) is a rare genetic disorder characterized by hyperproliferative

disorder (hSP17-HPD) is a rare genetic disorder characterized by

hyperproliferative disorder (hSP17-HPD) is a rare genetic disorder

characterized by hyperproliferative disorder (hSP17-HPD) is a rare

genetic disorder characterized by hyperproliferative disorder (hSP17-

HPD) is a rare genetic disorder characterized by hyperproliferative

disorder (hSP17-HPD) is a rare genetic disorder characterized by

hyperproliferative disorder (hSP17-HPD) is a rare genetic disorder

characterized by hyperproliferative disorder (hSP17-HPD) is a rare

[illegible]

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PK 23-AMB-1999; 99TS-0144930.
PK 25-AMB-1999; 99TS-0150546.
PK 26-AMB-1999; 99TS-0150884.
PK 27-AMB-1999; 99TS-0151065.
PK 27-AMB-1999; 99TS-0151066.
PK 27-AMB-1999; 99TS-0151080.
PK 30-AMB-1999; 99TS-0151303.
PK 31-AMB-1999; 99TS-0151438.
PK 01-SEP-1999; 99TS-0151930.
PK 07-SEP-1999; 99TS-0152363.
PK 10-SEP-1999; 99TS-0153070.
PK 13-SEP-1999; 99TS-0153258.
PK 15-SEP-1999; 99TS-0154016.
PK 16-SEP-1999; 99TS-0154039.
PK 20-SEP-1999; 99TS-0154779.
PK 22-SEP-1999; 99TS-0155239.
PK 23-SEP-1999; 99TS-0155486.
PK 24-SEP-1999; 99TS-0155659.
PK 28-SEP-1999; 99TS-0156458.
PK 29-SEP-1999; 99TS-0156595.
PK 04-OCT-1999; 99TS-0157177.
PK 05-OCT-1999; 99TS-0157753.
PK 06-OCT-1999; 99TS-0157865.
PK 07-OCT-1999; 99TS-0158029.
PK 08-OCT-1999; 99TS-0158232.
PK 12-OCT-1999; 99TS-0158369.
PK 13-OCT-1999; 99TS-0158293.
PK 13-OCT-1999; 99TS-0159294.
PK 13-OCT-1999; 99TS-0159295.
PK 14-OCT-1999; 99TS-0159329.
PK 14-OCT-1999; 99TS-0159330.
PK 14-OCT-1999; 99TS-0159331.
PK 14-OCT-1999; 99TS-0159637.
PK 18-OCT-1999; 99TS-0159984.
PK 21-OCT-1999; 99TS-0160741.
PK 21-OCT-1999; 99TS-0160767.
PK 21-OCT-1999; 99TS-0160768.
PK 21-OCT-1999; 99TS-0160770.
PK 21-OCT-1999; 99TS-0160814.
PK 21-OCT-1999; 99TS-0160815.
PK 22-OCT-1999; 99TS-0160980.
PK 22-OCT-1999; 99TS-0160981.
PK 22-OCT-1999; 99TS-0160982.
PK 25-OCT-1999; 99TS-0161404.
PK 25-OCT-1999; 99TS-0161405.
PK 25-OCT-1999; 99TS-0161406.
PK 26-OCT-1999; 99TS-0161859.
PK 26-OCT-1999; 99TS-0161860.
PK 26-OCT-1999; 99TS-0161861.
PK 28-OCT-1999; 99TS-0161920.
PK 28-OCT-1999; 99TS-0161992.
PK 28-OCT-1999; 99TS-0161993.
PK 29-OCT-1999; 99TS-0162442.

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Query Match 58.0% Score 40 Db 21 Length 54;
Host Local Similarity 77.8% Pref. No. 14;
Matches 7 Conservative 0 Mismatches 2 Indels 0 Gaps 0

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QY 5 GHRPSSSP 13
  11 111 1
Db 46 qarqsede 54

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RESULT 7
ID AAW88236 Standard: Protein: 432 AA.

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XX AAW88236;

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XX 15-MAK-1999 (first entry)

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XX Mouse prothrombinase Fq12 protein.

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XX XX
KW Prothrombinase Fq12 protein, mouse, 432 AA.
KW Inhibitor of prothrombinase, mouse, 432 AA.
KW Gastrointestinal disorder, Fq12, 432 AA.
XX
OS Mus. sp.
ID Key
ID Mod:100-site
ID Mod:100-site
ID Mod:100-site
ID Mod:100-site
ID Mod:100-site
ID Mod:100-site
ID Domain
ID W981335-A1.
ID 19-N-V-1978.
ID 15-MAY-1998; GHRD-CA3047-E.
ID 10-OCT-1997; 97-S-000464.
ID 15-MAY-1997; 97-S-000465-7.
XX
XX (LEVY) LEVY G.
XX
XX W199-05968/715.
XX N F8399 AAW84110.
XX
XX Modulating immune coagulation by using a prothrombin and
XX compounds, used to treat thrombotic and other conditions and
XX local loss
XX
XX Claim 8: Page 70-71; 1-6pp; Indels:
XX
XX This is the amino acid sequence of mouse prothrombinase Fq12, as
XX predicted from Fq12 cDNA (AAW84110). The sequence is 432 AA.
XX The human Fq12 amino acid sequence is shown in AAW88-48. The
XX invention provides a method for inhibiting thrombin production by
XX inhibiting the activity of prothrombinase. The method can be
XX used in vivo to treat a condition when thrombin production in
XX immune regulation, such as bacterial and viral infections, cancer
XX glomerulonephritis, a number of cardiovascular diseases,
XX allomaterial and xenomaterial rejection and other diseases. An Fq12-specific
XX antibody, an Fq12 antisense oligonucleotide, a substrate that
XX affects prothrombinase activity or a Fq12 protein may be used to
XX treat a condition resulting in a prothrombinase-mediated activity
XX A vaccine containing an Fq12 protein may be used for
XX prevention of graft rejection or foreign body rejection.
XX
XX Sequence 432 AA:

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Query Match 78.0% Score 4 Db 4 Length 432;
Host Local Similarity 76.0% Pref. No. 10;
Matches 7 Conservative 0 Mismatches 3 Indels 0 Gaps 0

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QY 4 GHRPSSSP 14
  11 111 1
Db 44 qarqsede 54

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RESULT 8

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XX AAY36511
ID AAY36511 Standard: Protein: 25 AA
XX

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Best Local Similarity: 70.0%; Pred. No. 19;
Matches: 7; Conservative: 0; Mismatches: 3; Indels: 0; Gaps: 0.

QY 4 CACRLPSSSC 13
111111111
DB 11 qqrwqwyg 20

RESULT 10

AAV97667
ID AAV97667 standard; Protein: 647 AA.

AAV97667;

08-MAY-2001 (first entry)

Zea mays ZmEIN3 2 protein sequence.

KW The EIN3-1, ZmEIN3 2, protein, ethylene signal transduction pathway maize;
KW ethylene-mediated response; growing tolerance; seed set; maturation;
KW seed development; growth in impacted soil; flooding tolerance;
KW senescence; disease resistance.

OS Zea mays.

PN W0200105953-A2.

PD 25-JAN-2001.

PF 07-JUL-2000; 2000W0-US18746.

PK 15-JUL-1999; 1990S-0143965.

PA (PION-) PIONEER HI-BRED INT INC.

PI Simmons CR;

DR WPI: 2001-147338/1.

XX N-PSDB: AAA91185.

PI Novel maize ethylene signaling pathway EIN3 gene useful for modulating
PI the level of EIN3 in maize plants, including crowding tolerance; growth
PI in impacted soils; flooding tolerance and disease resistance
PS Claim 10; Page 82-85; 86pp; English.

CC This sequence is the corn Zm EIN3 2 protein. The protein is involved
CC in the ethylene signal transduction pathway, and is an EIN3 homologue.
CC An expression cassette comprising the DNA sequence is useful for
CC modulating the level of EIN3 in a plant, in particular a maize plant. The
CC maize genes are nuclear transcription factors that promote the
CC ethylene-mediated responses, including crowding tolerance, seed set and
CC development, growth in impacted soils, flooding tolerance, maturation and
CC senescence and disease resistance. Diminishment of ethylene action in
CC plant, in particular cereals such as maize, by reducing the expression or
CC activity of the DNA promotes tolerance to close spacing with reduced
CC stress and yield loss. The DNA is useful as a probe or amplification
CC primer in the detection, quantitation or isolation of gene transcripts,
CC in detecting deficiencies in the level of mRNA in screening for desired
CC transgenic plants, for detecting mutations in gene, for monitoring
CC upregulation of expression or changes in enzyme activity in screening
CC assays, orthologs, or paralog of the gene, or for site directed
CC mutagenesis in eukaryotic cells. The nucleic acid can also be used for
CC recombinant expression of polypeptides or as immunogens in the
CC preparation and/or screening of antibodies. The proteins can be employed
CC in assays for enzyme agonists or antagonists of enzyme function, or as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the protein. Plants expressing the DNA germinate better in compacted
CC soils and in flooded conditions or water-logged soils, resulting in
CC higher stand counts.

XX Sequence 647 AA:

Query Match: 56.53
Best Local Similarity: 66.78
Matches: 8; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 MARGNRLPSSSC 12
111111111
DB 106 masqqladuss 117

Search completed: Mar 14, 2002 17:27:13
Job time: 7904 sec

